

Tab A

Applicant: John S. Lollar  
Appln. Serial No: 10/813,507  
Filing Date: March 30, 2004



Title: NUCLEIC ACID AND AMINO ACID SEQUENCES ENCODING HIGH-LEVEL  
EXPRESSOR FACTOR VIII POLYPEPTIDES AND METHODS OF USE

Appendix A

CLUSTAL W (1.82) multiple sequence alignment for SEQ ID NO: 15, 17, and 19

SEQIDNO\_15 . MQEELSTCVFLCLLPLGFSAIRRYYLGAVELSWDYRQSELLRELVHDTRFPATAPGALPL 60  
SEQIDNO\_19 . MQEELSTCVFLCLLPLGFSAIRRYYLGAVELSWDYRQSELLRELVHDTRFPATAPGALPL 60  
SEQIDNO\_17 . MQEELSTCVFLCLLPLGFSAIRRYYLGAVELSWDYRQSELLRELVHDTRFPATAPGALPL 60  
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SEQIDNO\_15 . GPSVLYKKTVFVEFTDQLFSVARPRPPWMGLGPTIQAEVYDTVVVTLKNMASHPVSLLHA 120  
SEQIDNO\_19 . GPSVLYKKTVFVEFTDQLFSVARPRPPWMGLGPTIQAEVYDTVVVTLKNMASHPVSLLHA 120  
SEQIDNO\_17 . GPSVLYKKTVFVEFTDQLFSVARPRPPWMGLGPTIQAEVYDTVVVTLKNMASHPVSLLHA 120  
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SEQIDNO\_15 . VGVSFWKSSSEGAEYYEDHTSQREKEDDKVLPGKSQTYWQVLKENGGPTASDPPCLTYSYL 180  
SEQIDNO\_19 . VGVSFWKSSSEGAEYYEDHTSQREKEDDKVLPGKSQTYWQVLKENGGPTASDPPCLTYSYL 180  
SEQIDNO\_17 . VGVSFWKSSSEGAEYYEDHTSQREKEDDKVLPGKSQTYWQVLKENGGPTASDPPCLTYSYL 180  
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SEQIDNO\_15 . HVDLVKDLDNSGLIGALLVCREGSLTRERTQNLFHEFVLLFAVDEGKSWHSARNDSWTRAM 240  
SEQIDNO\_19 . HVDLVKDLDNSGLIGALLVCREGSLTRERTQNLFHEFVLLFAVDEGKSWHSARNDSWTRAM 240  
SEQIDNO\_17 . HVDLVKDLDNSGLIGALLVCREGSLTRERTQNLFHEFVLLFAVDEGKSWHSARNDSWTRAM 240  
\*\*\*\*\*  
\*\*\*\*\*

SEQIDNO\_15 . DPAPARAQPAMHTVNGYVNRSLPGLIGCHKKSVYWHVIGMGTSPPEVHSIFLEGHTFLVRH 300  
SEQIDNO\_19 . DPAPARAQPAMHTVNGYVNRSLPGLIGCHKKSVYWHVIGMGTSPPEVHSIFLEGHTFLVRH 300  
SEQIDNO\_17 . DPAPARAQPAMHTVNGYVNRSLPGLIGCHKKSVYWHVIGMGTSPPEVHSIFLEGHTFLVRH 300  
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SEQIDNO_15.	HRQASLEISPLTFLTAQTFLMDQFLILFCHISSHHGGMEEAHVRVESCAEEPOLRRKAD	3 60
SEQIDNO_19.	HRQASLEISPLTFLTAQTFLMDQFLILFCHISSHHGGMEEAHVRVESCAEEPOLRRKAD	3 60
SEQIDNO_17.	HRQASLEISPLTFLTAQTFLMDQFLILFCHISSHHGGMEEAHVRVESCAEEPOLRRKAD	3 60

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SEQIDNO_15.	EEDDDNNLYDSDMDVRLGDDVSPPF1QIRSVAKHPKTWVHYIAEEEDWDYAPAVPS	420
SEQIDNO_19.	EEDDDNNLYDSDMDVRLGDDVSPPF1QIRSVAKHPKTWVHYIAEEEDWDYAPVLVA	420
SEQIDNO_17.	EEDDDNNLYDSDMDVRLGDDVSPPF1QIRSVAKHPKTWVHYIAEEEDWDYAPVLVA	420

SEQIDNO_15.	LIIIFQKASRPNLYIYPHGIDTVSALHPGRLLKWKHLKDMPILPGETFKYKWTVTVEDGP	540
SEQIDNO_19.	LIIIFQKQASRPNLYIYPHGIDTVRPLYSRRLPKGVKHLKDFPILPGEIFKYKWTVTVEDGP	540
SEQIDNO_17.	LIIIFQKQASRPNLYIYPHGIDTVRPLYSRRLPKGVKHLKDFPILPGEIFKYKWTVTVEDGP	540
*****;	*****;	*****;

SEQIDNO\_15.  
SEQIDNO\_19.  
SEQIDNO\_17.  
\*\*\*\*\*  
TKSDPRCLTRYSSINLEKDLASGLIGPLLICYKE  
SVDQRGNQMMSDKRNVLFLSFVFDE 600  
TKSDPRCLTRYSSFVNMERDLASGLIGPLLICYKE  
SVDQRGNQIMSDKRNVLFLSFVFDE 600  
TKSDPRCLTRYSSFVNMERDLASGLIGPLLICYKE  
SVDQRGNQIMSDKRNVLFLSFVFDE 600  
\*\*\*\*\*

SEQIDNO_15.	NNSWYLAENIQRFLPNPDGLQPQDPEFQASNIMHSINGYVFDSSLQLSVCLHEVAYWILS	660
SEQIDNO_19.	NRSWYLTENIQRFLPNPAGVQLEDPEFQASNIMHSINGYVFDSSLQLSVCLHEVAYWILS	660
SEQIDNO_17.	NRSWYLTENIQRFLPNPAGVQLEDPEFQASNIMHSINGYVFDSSLQLSVCLHEVAYWILS	660
*	*****	*****

SEQIDNO\_15.  
VGAQTDLSVFFSGYTFKHKKMVYEDTLIIFPFSGETVMSMENPGLWLGCHNSDLRNRG  
SEQIDNO\_19.  
IGAQTDLSVFFSGYTFKHKKMVYEDTLIIFPFSGETVMSMENPGLWLGCHNSDFRNRG  
SEQIDNO\_17.  
IGAQTDLSVFFSGYTFKHKKMVYEDTLIIFPFSGETVMSMENPGLWLGCHNSDFRNRG

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SEQIDNO_15.	SMGSNENIHSIFSGHVFSVRKKEEYKMAVNLYPGVFTETVEMILPSKGIVRIECLIGEH	1140
SEQIDNO_19.	SMGSNENIHSIFSGHVFSVRKKEEYKMAVNLYPGVFTETVEMILPSKGIVRIECLIGEH	1140
SEQIDNO_17.	SMGSNENIHSIFSGHVFSTVRKKEEYKMAVNLYPGVFTETVEMILPSKGIVRVECLIGEH	1130
	*****	*****

SEQIDNO_15.	LQAGMSTFLVYSKCKQTPLGMASGHIRDFOITASGGQYQWAPKLARLYHGSINAWSTK	1200
SEQIDNO_19.	LQAGMSTFLVYSKCKQTPLGMASGHIRDFOITASGGQYQWAPKLARLYHGSINAWSTK	1200
SEQIDNO_17.	LHAGMSTFLVYSNKCKQTPLGMASGHIRDFOITASGGQYQWAPKLARLYHGSINAWSTK	1190
*	*****;	*****;

SEQIDNO\_15 . EPFSWIKVDLLAPMIIHGKTKQARQKFSSLYISQFIIIMYSLDGKKWQTYGNSTGTLMV 1260  
 SEQIDNO\_19 . EPFSWIKVDLLAPMIIHGKTKQARQKFSSLYISQFIIIMYSLDGKKWQTYGNSTGTLMV 1260  
 SEQIDNO\_17 . EPFSWIKVDLLAPMIIHGKTKQARQKFSSLYISQFIIIMYSLDGKKWQTYGNSTGTLMV 1250  
 \*\*\*\*  
 \*\*\*\*  
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SEQIDNO\_15. SDAQITASSYFTNMFMATWSPSKARLHLQGRSNAWRPQVNPKEWLQVDFQKTMKVTVGVT  
 SEQIDNO\_19. SDAQITASSYFTNMFMATWSPSKARLHLQGRSNAWRPQVNPKEWLQVDFQKTMKVTVGVT  
 SEQIDNO\_17. SDAQITASSYFTNMFMATWSPSKARLHLQGRSNAWRPQVNPKEWLQVDFQKTMKVTVGVT  
 \*\*\*\*  
 \*\*\*\*

SEQIDNO\_15.  
QGVKSLLTSMYVKEFLISSQDGHQWTLFQNGKVKVFGQNQDSFTPVVNSLDPLILRY 1440  
SEQIDNO\_19.  
QGVKSLLTSMYVKEFLISSQDGHQWTLFQNGKVKVFGQNQDSFTPVVNSLDPLILRY 1440  
SEQIDNO\_17.  
QGVKSLLTSMYVKEFLISSQDGHQWTLFQNGKVKVFGQNQDSFTPVVNSLDPLILRY 1430

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SEQIDNO\_15. LRIHPQSWVHQIALRMEVLGCEAQDLY 1467  
SEQIDNO\_19. LRIHPQSWVHQIALRMEVLGCEAQDLY 1467  
SEQIDNO\_17. LRIHPQSWVHQIALRMEVLGCEAQDLY 1457  
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APPENDIX B

CLUSTAL W (1.82) multiple sequence alignment for SEQ ID NO: 14, 16, and 18

SEQIDNO\_14  
SEQIDNO\_18  
SEQIDNO\_16  
\*\*\*\*\*

ATGCAGCTAGAGCTCTCCACCTGTCTTCTGRTGTCCTGGCAACTCGGCTTTAGTGCC 60  
ATGCAGCTAGAGCTCTCCACCTGTCTTCTGRTGTCCTGGCAACTCGGCTTTAGTGCC 60  
ATGCAGCTAGAGCTCTCCACCTGTCTTCTGRTGTCCTGGCAACTCGGCTTTAGTGCC 60  
\*\*\*\*\*

SEQIDNO\_14  
SEQIDNO\_18  
SEQIDNO\_16  
\*\*\*\*\*

ATCAGGAGATACTACTCTGGGGCAGTGGAAACTACGGGACTACGGCAAAGTGAACTC 120  
ATCAGGAGATACTACTCTGGGGCAGTGGAAACTACGGGACTACGGCAAAGTGAACTC 120  
ATCAGGAGATACTACTCTGGGGCAGTGGAAACTACGGGACTACGGCAAAGTGAACTC 120  
\*\*\*\*\*

SEQIDNO\_14  
SEQIDNO\_18  
SEQIDNO\_16  
\*\*\*\*\*

CTCCGTGAGCTGCACGTGGACACCAAGATTCTGCTACAGGCCAGGAGCTCTTCCGTTG 180  
CTCCGTGAGCTGCACGTGGACACCAAGATTCTGCTACAGGCCAGGAGCTCTTCCGTTG 180  
CTCCGTGAGCTGCACGTGGACACCAAGATTCTGCTACAGGCCAGGAGCTCTTCCGTTG 180  
\*\*\*\*\*

SEQIDNO\_14  
SEQIDNO\_18  
SEQIDNO\_16  
\*\*\*\*\*

GGCCCGTCAAGTCCGTACAAAAAGACTGTGTTCGTAGAGTTCACGGATCAACTTTTCAGC 240  
GGCCCGTCAAGTCCGTACAAAAAGACTGTGTTCGTAGAGTTCACGGATCAACTTTTCAGC 240  
GGCCCGTCAAGTCCGTACAAAAAGACTGTGTTCGTAGAGTTCACGGATCAACTTTTCAGC 240  
\*\*\*\*\*

SEQIDNO\_14  
SEQIDNO\_18  
SEQIDNO\_16  
\*\*\*\*\*

GTTGCCAGGCCACCATGGATGGGTCTGCTGGGTCTGCTGGGTCTGCTGGGTCTGCTGGGT 300  
GTTGCCAGGCCACCATGGATGGGTCTGCTGGGTCTGCTGGGTCTGCTGGGTCTGCTGGGT 300  
GTTGCCAGGCCACCATGGATGGGTCTGCTGGGTCTGCTGGGTCTGCTGGGTCTGCTGGGT 300  
\*\*\*\*\*

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SEQIDNO\_14 TACGACACGGTGGTACCGTGAAGAACATGGCTCTCATCCCGTTAGTCCTCACGCT 360  
SEQIDNO\_18 TAGACACGGTGGTACCGTGAAGAACATGGCTCTCATCCCGTTAGTCCTCACGCT 360  
SEQIDNO\_16 TAGACACGGTGGTACCGTGAAGAACATGGCTCTCATCCCGTTAGTCCTCACGCT 360  
\*\*\*\*\*

SEQIDNO\_14 GTCGGGCGTCTCCTCTGGAAATTCTCCGAAGGGCCTGAATAATGAGGATCACACCAGCAA 420  
SEQIDNO\_18 GTCGGGCGTCTCCTCTGGAAATTCTCCGAAGGGCCTGAATAATGAGGATCACACCAGCAA 420  
SEQIDNO\_16 GTCGGGCGTCTCCTCTGGAAATTCTCCGAAGGGCCTGAATAATGAGGATCACACCAGCAA 420  
\*\*\*\*\*

SEQIDNO\_14 AGGGAGAAGGAAGACGATAAAGTCCTTCCCGTAAAGCCAAAACCTACGTCTGGCAGGTC 480  
SEQIDNO\_18 AGGGAGAAGGAAGACGATAAAGTCCTTCCCGTAAAGCCAAAACCTACGTCTGGCAGGTC 480  
SEQIDNO\_16 AGGGAGAAGGAAGACGATAAAGTCCTTCCCGTAAAGCCAAAACCTACGTCTGGCAGGTC 480  
\*\*\*\*\*

SEQIDNO\_14 CTGAAGAAAATGGTCCAACGCCACCATGGCCTCTGACCCATGTCTTAACCTACTCATACCTGTCT 540  
SEQIDNO\_18 CTGAAGAAAATGGTCCAACGCCACCATGGCCTCTGACCCACATGTCTTAACCTACTCATACCTGTCT 540  
SEQIDNO\_16 CTGAAGAAAATGGTCCAACGCCACCATGGCCTCTGACCCACATGTCTTAACCTACTCATACCTGTCT 540  
\*\*\*\*\*

SEQIDNO\_14 CACGTGGACCTGGAAAGACCTGAATTGGGGCCTCATGGAGCCCTGCTGGTTGTAGA 600  
SEQIDNO\_18 CACGTGGACCTGGTGAAGACCTGAATTGGGGCCTCATGGAGCCCTGCTGGTTGTAGA 600  
SEQIDNO\_16 CACGTGGACCTGGTGAAGACCTGAATTGGGGCCTCATGGAGCCCTGCTGGTTGTAGA 600  
\*\*\*\*\*

SEQIDNO\_14 GAAGGGAGTCTGACCAAGAGAACGGACCCAGAACCTGCACGAATTGTACTACCTTTTGCT 660  
SEQIDNO\_18 GAAGGGAGTCTGACCAAGAGAACGGACCCAGAACCTGCACGAATTGTACTACCTTTTGCT 660  
SEQIDNO\_16 GAAGGGAGTCTGACCAAGAGAACGGACCCAGAACCTGCACGAATTGTACTACCTTTTGCT 660  
\*\*\*\*\*

SEQIDNO\_14 GTCTTTGATGAAGGAAAGTGGCACTCAGCAAGAAATGACTCCTGGACACGGCCATG 720  
SEQIDNO\_18 GTCTTTGATGAAGGAAAGTGGCACTCAGCAAGAAATGACTCCTGGACACGGCCATG 720  
SEQIDNO\_16 GTCTTTGATGAAGGAAAGTGGCACTCAGCAAGAAATGACTCCTGGACACGGCCATG 720  
\*\*\*\*\*

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SEQIDNO\_14 GATCCCCGACCTGCCAAGGGCCCAGCCTGCATAATGCCACACAGTCAAATGGCTATGTCAAACAGG 780  
SEQIDNO\_18 GATCCCCGACCTGCCAAGGGCCCAGCCTGCATAATGCCACACAGTCAAATGGCTATGTCAAACAGG 780  
SEQIDNO\_16 GATCCCCGACCTGCCAAGGGCCCAGCCTGCATAATGCCACACAGTCAAATGGCTATGTCAAACAGG 780  
\*\*\*\*\*  
\*\*\*\*\*

SEQIDNO\_14 TCTCTGCCAGGTCTGATGGATGTCATAAGAAATCAGTCTACTGGCACCGTGAATTGAAATG 840  
SEQIDNO\_18 TCTCTGCCAGGTCTGATGGATGTCATAAGAAATCAGTCTACTGGCACCGTGAATTGAAATG 840  
SEQIDNO\_16 TCTCTGCCAGGTCTGATGGATGTCATAAGAAATCAGTCTACTGGCACCGTGAATTGAAATG 840  
\*\*\*\*\*  
\*\*\*\*\*

SEQIDNO\_14 GGCACCAAGCCCCGAAAGTGCACCTCCATTTTCTTGAGGGCCACACGGTTTCCTGTGAGGCAC 900  
SEQIDNO\_18 GGCACCAAGCCCCGAAAGTGCACCTCCATTTCCTTGAGGGCCACACGGTTTCCTGTGAGGCAC 900  
SEQIDNO\_16 GGCACCAAGCCCCGAAAGTGCACCTCCATTTCCTTGAGGGCCACACGGTTTCCTGTGAGGCAC 900  
\*\*\*\*\*  
\*\*\*\*\*

SEQIDNO\_14 CATGCCAGGCTTCCCTGGAGATCTGCCACATAACTTCTCAGACATTCCCTG 960  
SEQIDNO\_18 CATGCCAGGCTTCCCTGGAGATCTGCCACATAACTTCTCAGACATTCCCTG 960  
SEQIDNO\_16 CATGCCAGGCTTCCCTGGAGATCTGCCACATAACTTCTCAGACATTCCCTG 960  
\*\*\*\*\*  
\*\*\*\*\*

SEQIDNO\_14 ATGGACCTTGGCCAGTTCCCTACTGTTTGTCAATATCTCTCCACACCATTGGGGCATG 1020  
SEQIDNO\_18 ATGGACCTTGGCCAGTTCCCTACTGTTTGTCAATATCTCTCCACACCATTGGGGCATG 1020  
SEQIDNO\_16 ATGGACCTTGGCCAGTTCCCTACTGTTTGTCAATATCTCTCCACACCATTGGGGCATG 1020  
\*\*\*\*\*  
\*\*\*\*\*

SEQIDNO\_14 GAGGCTCACGTCAGGTAGAAAGCTGGCCAGGAGCCCCAGCTGGGAGAAAGCTGAT 1080  
SEQIDNO\_18 GAGGCTCACGTCAGGTAGAAAGCTGGCCAGGAGCCCCAGCTGGGAGAAAGCTGAT 1080  
SEQIDNO\_16 GAGGCTCACGTCAGGTAGAAAGCTGGCCAGGAGCCCCAGCTGGGAGAAAGCTGAT 1080  
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SEQIDNO\_14 GAAGAGGAAGATTATGATGACAATTGGTACCGACTCGGACATGGACGTGGCCGGCTCGAT 1140  
SEQIDNO\_18 GAAAGAGGAAGATTATGATGACAATTGGTACCGACTCGGACATGGACGTGGCCGGCTCGAT 1140  
SEQIDNO\_16 GAAGAGGAAGATTATGATGACAATTGGTACCGACTCGGACATGGACGTGGCCGGCTCGAT 1140  
\*\*\*\*\*  
SEQIDNO\_14 GGTGACCGACGTGTCTCCCTTATCCAATCCGCTCGGGACTACGCCAAGAACCATCCC 1200  
SEQIDNO\_18 GGTGACCGACGTGTCTCCCTTATCCAATCCGCTCAGTTGCCAAGAACCATCTAAACT 1200  
SEQIDNO\_16 GGTGACCGACGTGTCTCCCTTATCCAATCCGCTCAGTTGCCAAGAACCATCTAAACT 1200  
\*\*\*\*\*  
SEQIDNO\_14 TGGGTGCACTACATCTGCAGAGGGAGGACTGGGACTCTACTTGAAACAGTGGTCTCAGCGA 1260  
SEQIDNO\_18 TGGGTACATTACATGGCTGCTGAAGAGGAGCACTGGGACTATGGCTCCCTTAGTCCTCGCC 1260  
SEQIDNO\_16 TGGGTACATTACATGGCTGCTGAAGAGGAGCACTGGGACTATGGCTCCCTTAGTCCTCGCC 1260  
\*\*\*\*\*  
SEQIDNO\_14 CCCAGTGACAGAAGTTAAAAGTCTACTTGAAACAGTGGTCTCAGCGAATTGGTAGG 1320  
SEQIDNO\_18 CCCGATGACAGAAGTTAAAAGTCAATATTGAAACAAATGGCCCTCAGCGGATTGGTAGG 1320  
SEQIDNO\_16 CCCGATGACAGAAGTTAAAAGTCAATATTGAAACAAATGGCCCTCAGCGGATTGGTAGG 1320  
\*\*\*\*\*  
SEQIDNO\_14 AAATACAAAAAGCTGATTCTGCCTTACACGGATGTAACATTAAAGACTCGTAAAGCT 1380  
SEQIDNO\_18 AAGTACAAAAAGTCGATTATGGCATAACACAGATGAAACCTTAAAGCGCTGAAGCT 1380  
SEQIDNO\_16 AAGTACAAAAAGTCGATTATGGCATAACACAGATGAAACCTTAAAGCGCTGAAGCT 1380  
\*\*\*\*\*  
SEQIDNO\_14 ATTCCGTTGATGAAATCGGAATCCTGGACCTTACTTTATGGAGAACCTGGACACACTT 1440  
SEQIDNO\_18 ATTCAGCATGAAATCGGAATCTTGGGACCTTACTTTATGGGAAGTTGGACACACTG 1440  
SEQIDNO\_16 ATTCAGCATGAAATCGGAATCTTGGGACCTTACTTTATGGGAAGTTGGACACACTG 1440  
\*\*\*\*\*  
SEQIDNO\_14 TTGATTATATTAAAGATAAGGAGCCATATAACATCTACCCCTCATGGAATCACT 1500  
SEQIDNO\_18 TTGATTATATTAAAGATAAGGAGCCATATAACATCTACCCCTCATGGAATCACT 1500  
SEQIDNO\_16 TTGATTATATTAAAGATAAGGAGCCATATAACATCTACCCCTCATGGAATCACT 1500

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SEQIDNO_14	CAGCCCCAGGATCCAGAGTTCAAGCTTCAACATCATGGCTATGTT	1920
SEQIDNO_18	CAGCTTGGGATCCAGAGTTCAAGCTTCAACATCATGGCTATGTT	1920
SEQIDNO_16	CAGCTTGGGATCCAGAGTTCAAGCTTCAACATCATGGCTATGTT	1920
	*****	*****

SEQIDNO_	14	TTTGATAGCTTGCAGGTGTCGGTTGCAAGAGCTGGCATACTGGTACATTCTAAGT	1980
SEQIDNO_	18	TTTGATAGTTGCAGTTGTCAGTTGCTGATGAGTGGCATACTGGTACATTCTAAGC	1980
SEQIDNO_	16	TTTGATAGTTGCAGTTGTCAGTTGCTGATGAGTGGCATACTGGTACATTCTAAGC	1980
	*	*****	*****

SEQIDNO_14	GTTGGAGCACAGACGGACTTCTCCGCTTCTGGCTACACCTCAAACACAAA	2040
SEQIDNO_18	ATTGGAGCACAGACTGACTTCTCTGGATATACTTCAAACACAAA	2040
SEQIDNO_16	ATTGGAGCACAGACTGACTTCTCTGGATATACTTCAAACACAAA	2040
	*****	

SEQIDNO_14	ATGGTCTATGAAGACACACTCACCCCTTCAGGAAACGGTTCATGCA	2100
SEQIDNO_18	ATGGTCTATGAAGACACACTCACCCATTCCATTTCAGGAAACTGTG	2100
SEQIDNO_16	ATGGTCTATGAAGACACACTCACCCATTTCAGGAAACTGTGCG	2100
	*****	

SEQIDNO_14	ATGGAAAACCCAGGTCTTGGGTGCCACAACTCAGACTTGGGAACAGAGGG	2160
SEQIDNO_18	ATGGAAAACCCAGGTCTATGGATTCTGGGTGCCACAACTCAGACTTGGAACAGAGGC	2160
SEQIDNO_16	ATGGAAAACCCAGGTCTATGGATTCTGGGTGCCACAACTCAGACTTGGAACAGAGGC	2160
*****		

SEQIDNO_14	ATGACAGCCCTACTGAAGGTGTTAGTGTGACAGGACATTGGTGATTATATGACAAC	2220
SEQIDNO_18	ATGACGCCCTACTGAAGGTGTTCTAGTGTGACAAGAACACTGGTGATTATACGAGGAC	2220
SEQIDNO_16	ATGACGCCCTACTGAAGGTGTTCTAGTGTGACAAGAACACTGGTGATTATACGAGGAC	2220
	*****	*****

SEQIDNO_14	ACTTATGAAAGATAATTCCAGGCTTCTTGCTGAGTGGAAAAGAATGTCAATTGAAACCTAGGAGC	2280
SEQIDNO_18	AGTTATGAAAGATAATTTCAGGCATACTTGTGACTAAACAAATGCCATTGAAACCTAGGAGC	2280
SEQIDNO_16	AGTTATGAAAGATAATTTCAGGCATACTTGTGAGTAAAACAATGCCATTGAAACCTAGGAGC	2280

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SEQIDNO\_14 CCGTCGTACGGGGAACTCAACAAACACTGGGCTACTTGGGACCCATAGAGCG 2700

SEQIDNO\_18 CCGTCGTACGGGGAACTCAACAAACACTGGGCTACTTGGGACCCATAGAGCG 2700

SEQIDNO\_16 CCCTTATACCGGGAGAACATAATGAACATTGGGACTCCTGGGCCATATAAGAGCA 2670

\* \*

SEQIDNO\_14 GAAGTTGAAGACAACATCATGGTAACTTCAAAAACCAGGGCGTCGTCCTATTCCCTTC 2760

SEQIDNO\_18 GAAGTTGAAGACAACATCATGGTAACTTCAAAAACCAGGGCGTCGTCCTATTCCCTTC 2760

SEQIDNO\_16 GAAGTTGAAGATAATATCATGGTAACTTCAAAAATCAGGGCTTCGTCCTATTCCCTTC 2730

\* \*

SEQIDNO\_14 TACTCGAGCCTTATTCTTATCCGGATGATCAGGAGCAAGGGCAGAACCTCGACACAAAC 2820

SEQIDNO\_18 TACTCGAGCCTTATTCTTATCCGGATGATCAGGAGCAAGGGCAGAACCTCGACACAAAC 2820

SEQIDNO\_16 TATTCTAGCCTTATTCTTATGAGGAAGATCAGGGCAAGGAGCAACCTAGAAAAAAC 2790

\* \*

SEQIDNO\_14 TTTCGTCCAGCCAATGAAACCGAAACTTACTTTGGAAAGTGCAGCATCACGGCACCC 2880

SEQIDNO\_18 TTTCGTCCAGCCAATGAAACCGAAACTTACTTTGGAAAGTGCAGCATCACGGCACCC 2880

SEQIDNO\_16 TTTCGTCAAGGCCATTATGAAACCCAAACTTACTTTGGAAAGTGCACATCATGGCACCC 2850

\* \*

SEQIDNO\_14 ACAGAAAGACGAGTTGACTGCAAAGCCTGGGCCACTTTCTGATGTTGACCTGGAAAAA 2940

SEQIDNO\_18 ACAGAAAGACGAGTTGACTGCAAAGCCTGGGCCACTTTCTGATGTTGACCTGGAAAAA 2940

SEQIDNO\_16 ACTAAAGATGAGTTGACTGCAAAGCCTGGCCATTTCCTGATGTTGACCTGGAAAAA 2910

\* \*

SEQIDNO\_14 GATGTGCACTCAGGCCATTGATGGCCCCCTTGATCTGGCGCCAACACCCCTGAACGCT 3000

SEQIDNO\_18 GATGTGCACTCAGGCCATTGATGGCCCCCTTGATCTGGCGCCAACACCCCTGAACGCT 3000

SEQIDNO\_16 GATGTGCACTCAGGCCATTGATGGCCCCCTTGATCTGGCGCCAACACCCCTGAACGCT 2970

\* \*

SEQIDNO\_14 GCTCACGGTAGACAAGTGCACCGGTGCAAGAAATTGCTCTGTTTCACTATTGAG 3060

SEQIDNO\_18 GCTCACGGTAGACAAGTGCACCGGTGCAAGAAATTGCTCTGTTTCACTATTGAG 3060

SEQIDNO\_16 GCTCATGGGAGACAAGTGCACAGTACAGGAATTGCTCTGTTTCACTATTGAG 3030

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SEQIDNO\_14    ACAAAAGAGCTGGTACTTCACTGAAATGTGAAAGGAACACTGCCGCCCCCTGCCATCTG 3120  
SEQIDNO\_18    ACAAAAGAGCTGGTACTTCACTGAAAATGTGAAAGGAACACTGCCGCCCCCTGCCATCTG 3120  
SEQIDNO\_16    ACCAAAAGCTGGTACTTCACTGAAAATATGGAAAGAACACTGCAGGGCTCCCTGCAATATC 3090  
\*\*\*\*\*  
  
SEQIDNO\_14    CAGATGGAGGACCCCACCTCTGAAAGAAAACATCGCTTCCATGCCAATCAATGGCTATGTG 3180  
SEQIDNO\_18    CAGATGGAGGACCCCACCTCTGAAAGAAAACATCGCTTCCATGCCAATCAATGGCTATGTG 3180  
SEQIDNO\_16    CAGATGGAAAGATCCCACTTTAAGAGAAATTATCGCTTCCATGCCAATCAATGGCTACATA 3150  
\*\*\*\*\*  
  
SEQIDNO\_14    ATGGATAACACTCCCTGGCTTAGTAATGGCTCAGAATCAAAGGATCAGTGCTC 3240  
SEQIDNO\_18    ATGGATAACACTCCCTGGCTTAGTAATGGCTCAGAATCAAAGGATCAGTGCTC 3240  
SEQIDNO\_16    ATGGATAACACTACCTGGCTTAGTAATGGCTCAGGATCAAAGGATTGATGGTATCTGCTC 3210  
\*\*\*\*\*  
  
SEQIDNO\_14    AGCATGGGCAGCAATGAAATATCCATTGCAATTGCTTACAGTGTTCAAGTGTA 3300  
SEQIDNO\_18    AGCATGGGCAGCAATGAAATATCCATTGCAATTGCTTACAGTGTTCAAGTGTA 3300  
SEQIDNO\_16    AGCATGGGCAGCAATGAAACATCCATTCTATTCACTGGACATGTGTTCACTGTGTA 3270  
\*\*\*\*\*  
  
SEQIDNO\_14    CGGAAAAAGGAGGAGTATAAAATGCCGTACAATCTCTATCCGGGTGCTTGTGAGACA 3360  
SEQIDNO\_18    CGGAAAAAGGAGGAGTATAAAATGCCGTACAATCTCTATCCGGGTGCTTGTGAGACA 3360  
SEQIDNO\_16    CGGAAAAAGGAGGAGTATAAAATGCCACTGACAATCTCTATCCGGGTGCTTGTGAGACA 3330  
\*\*\*\*\*  
  
SEQIDNO\_14    GTGGAAATGCTACCGTCCAAGTTGGGAATTAGAATGCTGATTGGCAGCAC 3420  
SEQIDNO\_18    GTGGAAATGCTACCGTCCAAGTTGGGAATTAGAATGCTGATTGGCAGCAC 3420  
SEQIDNO\_16    GTGGAAATGTTACCATCCAAAGCTGGAAATTGGGGTGGAAATGCTTATTGGCAGCAT 3390  
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Appln. Serial No: 10/813,507  
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**Title:** NUCLEIC ACID AND AMINO ACID SEQUENCES ENCODING HIGH-LEVEL EXPRESSION FACTOR VIII POLYPEPTIDES AND METHODS OF USE

SEQIDNO_14	CTGCAAGCTGGATGAGCACCGACTTCCGTACAGCAAGAAGTGTCAAGACTCCCCCTG	3 480
SEQIDNO_18	CTGCAAGCTGGATGAGCACCGACTTCCGTACAGCAAGAAGTGTCAAGACTCCCCCTG	3 480
SEQIDNO_16	CTACATCGCTGGATGAGCACACCTTTCTGGTACAGCAATAAGTGTCAAGACTCCCCCTG	3 450
*****	*****	*****
SEQIDNO_14	GGAATGGCTTCTGGACACATTAGAGATTTCAGATTACAGCTTACGGACAATATGGACAG	3 540
SEQIDNO_18	GGAATGGCTTCTGGACACATTAGAGATTTCAGATTACAGCTTACGGACAATATGGACAG	3 540
SEQIDNO_16	GGAATGGCTTCTGGACACATTAGAGATTTCAGATTACAGCTTACGGACAATATGGACAG	3 510
*****	*****	*****
SEQIDNO_14	TGGCCCCCAAAGCTGGCCAGACTTCATTTCGGATCAATCAATGCCTGGAGCCAAG	3 600
SEQIDNO_18	TGGCCCCCAAAGCTGGCCAGACTTCATTTCGGATCAATCAATGCCTGGAGCCAAG	3 600
SEQIDNO_16	TGGCCCCCAAAGCTGGCCAGACTTCATTTCGGATCAATCAATGCCTGGAGCCAAG	3 570
*****	*****	*****
SEQIDNO_14	GAGGCCCTTTCTGGATCAAGGGGGATCTGGCCAAATGATTTCAGGGCATCAAG	3 660
SEQIDNO_18	GAGGCCCTTTCTGGATCAAGGGGGATCTGGCCAAATGATTTCAGGGCATCAAG	3 660
SEQIDNO_16	GAGGCCCTTTCTGGATCAAGGGGGATCTGGCCAAATGATTTCAGGGCATCAAG	3 630
*****	*****	*****
SEQIDNO_14	ACCCAGGGTGCCCGTCAGAAGTTCTCCAGCCTCTACATCTCTCAGTTTATCATGTAT	3 720
SEQIDNO_18	ACCCAGGGTGCCCGTCAGAAGTTCTCCAGCCTCTACATCTCTCAGTTTATCATGTAT	3 720
SEQIDNO_16	ACCCAGGGTGCCCGTCAGAAGTTCTCCAGCCTCTACATCTCTCAGTTTATCATGTAT	3 690
*****	*****	*****
SEQIDNO_14	AGTCTTGATGGAAAGAAGTGGCAGACTTATCGAGGAATTCCACTGGAACCTTAATGGTC	3 780
SEQIDNO_18	AGTCTTGATGGAAAGAAGTGGCAGACTTATCGAGGAATTCCACTGGAACCTTAATGGTC	3 780
SEQIDNO_16	AGTCTTGATGGAAAGAAGTGGCAGACTTATCGAGGAATTCCACTGGAACCTTAATGGTC	3 750
*****	*****	*****

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EXPRESSOR FACTOR VIII POLYPEPTIDES AND METHODS OF USE

SEQIDNO\_14 TTCTTTGGCAATGTGATTCATCTGGGATAAAACACAATATTTCACCCCTCATTATT 3840  
SEQIDNO\_18 TTCTTTGGCAATGTGATTCATCTGGGATAAAACACAATATTTCACCCCTCATTATT 3840  
SEQIDNO\_16 TTCTTTGGCAATGTGATTCATCTGGGATAAAACACAATATTTCACCCCTCATTATT 3810  
\*\*\*\*\*

SEQIDNO\_14 GCTCGATACATCCGTTGCACCCAACCTCATATAAGCATTGCAGCACTCTTGCATGGAG 3900  
SEQIDNO\_18 GCTCGATACATCCGTTGCACCCAACCTCATATAAGCATTGCAGCACTCTTGCATGGAG 3900  
SEQIDNO\_16 GCTCGATACATCCGTTGCACCCAACCTCATATAAGCATTGCAGCACTCTTGCATGGAG 3870  
\*\*\*\*\*

SEQIDNO\_14 TTGATGGGCTGTGATTAAATAAGTGGCAGCATGGGAATGGAGAGTAAAGCAATA 3960  
SEQIDNO\_18 TTGATGGGCTGTGATTAAATAAGTGGCAGCATGGGAATGGAGAGTAAAGCAATA 3960  
SEQIDNO\_16 TTGATGGGCTGTGATTAAATAAGTGGCAGCATGGGAATGGAGAGTAAAGCAATA 3930  
\*\*\*\*\*

SEQIDNO\_14 TCAGATGCACAGATTACTGCTTCATCCTACTTTACCAATAATGTTGCCACCTGGTCTCCT 4020  
SEQIDNO\_18 TCAGATGCACAGATTACTGCTTCATCCTACTTTACCAATAATGTTGCCACCTGGTCTCCT 4020  
SEQIDNO\_16 TCAGATGCACAGATTACTGCTTCATCCTACTTTACCAATAATGTTGCCACCTGGTCTCCT 3990  
\*\*\*\*\*

SEQIDNO\_14 TCAAAAGCTCGACTTCACCTCCAGGGAGGTAATGCCCTGGAGACCTCAGGTGAATAAT 4080  
SEQIDNO\_18 TCAAAAGCTCGACTTCACCTCCAGGGAGGTAATGCCCTGGAGACCTCAGGTGAATAAT 4080  
SEQIDNO\_16 TCAAAAGCTCGACTTCACCTCCAGGGAGGTAATGCCCTGGAGACCTCAGGTGAATAAT 4050  
\*\*\*\*\*

SEQIDNO\_14 CCAAAAGACTGGCTGCAAGTGGACCTCCAGAAGACAATGAAAAGTCAACAGGAGTAACTACT 4140  
SEQIDNO\_18 CCAAAAGACTGGCTGCAAGTGGACCTCCAGAAGACAATGAAAAGTCAACAGGAGTAACTACT 4140  
SEQIDNO\_16 CCAAAAGACTGGCTGCAAGTGGACCTCCAGAAGACAATGAAAAGTCAACAGGAGTAACTACT 4110  
\*\*\*\*\*

SEQIDNO\_14 CAGGGAGTAAAATCTCTGCTTACAGGATGATGTAAGGAGTTCTCTCATCTCCAGCAGT 4200  
SEQIDNO\_18 CAGGGAGTAAAATCTCTGCTTACAGGATGATGTAAGGAGTTCTCTCATCTCCAGCAGT 4200  
SEQIDNO\_16 CAGGGAGTAAAATCTCTGCTTACAGGATGATGTAAGGAGTTCTCTCATCTCCAGCAGT 4170  
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SEQIDNO_	14	CAAGATGCCATCAGTGGACTCTCTTTTCAAGATTGCAAAGTAAGGTTTTTCAGGA	4260
SEQIDNO_	18	CAAGATGCCATCAGTGGACTCTCTTTTCAAGATTGCAAAGTAAGGTTTTTCAGGA	4260
SEQIDNO_	16	CAAGATGCCATCAGTGGACTCTCTTTTCAAGATTGCAAAGTAAGGTTTTTCAGGA	4230
		*****	*****

SEQIDNO_14	AATCAAGACTCCTTACACCTGTGGTGA ACTCTAGACCACCGTTACTGACTCGCTAC	4320
SEQIDNO_18	AATCAAGACTCCTTACACCTGTGGTGA ACTCTAGACCACCGTTACTGACTCGCTAC	4320
SEQIDNO_16	AATCAAGACTCCTTACACCTGTGGTGA ACTCTAGACCACCGTTACTGACTCGCTAC	4290
	*****	*****

SEQIDNO_14	CTTCGAATTACCCCCAGAGTGGGTGCAACCAGATTGCCCTGAGGATGGAGCTTCTGGGC	4380
SEQIDNO_18	CTTCGAATTACCCCCAGAGTGGGTGCAACCAGATTGCCCTGAGGATGGAGCTTCTGGGC	4380
SEQIDNO_16	CTTCGAATTACCCCCAGAGTGGGTGCAACCAGATTGCCCTGAGGATGGAGCTTCTGGGC	4350
*	*****	*

SEQIDNO_14	TGGAGGCACAGGACCTCTAC	4401
SEQIDNO_18	TGGAGGCACAGGACCTCTAC	4401
SEQIDNO_16	TGGAGGCACAGGACCTCTAC	4371
	*****	*****